

INFORMAL SEQUENCE LISTING

SEQ ID NO:1

Wild type DT with signal sequence underlined

5 GTGAGCAGAAAACTGTTGCGTCAATCTTAATAGGGCGCTACTGGGATAGGGCCACCTCAGCCCATGCA
 GGCCTGATGATGTTGATTCTCTAAATCTTGATGGAAAACCTTCCTCGTACACAGGAAACTGACGATGATTGG
 GGTTATGTAGATTCCATTCAAAAAGGTATAACAAAGCAAATCTGGTACACAAGGAATTATGACGATGATTGG
 AAAGGGTTTATAGTACCGACAATAAATACGACGCTGCCGACTCTGTAGATAATGAAAACCGCTCTGGAA
 AAAGCTGGAGGCCTGGTCAAAGTACGTATCCAGGACTGACGAAGGTTCTGCACTAAAAGTGGATAATGCCGAA
 10 ACTATTAAGAAAAGAGTTAGGTTAACGTCACTGAACCGTTGATGGAGCAAGTCGGAACGGAAGAGTTATCAAA
 AGGTCGGTATGGTCTCGCGTGTAGTGCTCAGCCTCCCTCGCTGAGGGAGTTCTAGCGTTGAATATATT
 AATAACTGGGAAACAGGGAAAGCGTTAACGCTAGAACATTGAGATAATTTGAAACCCGTGGAAAACGTGCCAA
 GATGCGATGTATGAGTATATGGCTCAAGCCTGTGCAGGAAATCGTGTCAAGGCGATCAGTAGGTAGCTCATTGTCA
 TGCATAAAATCTTGATTGGATGTCATAAGGGATAAAACTAACAGACAAAGATAAGTCTTGAAGAGCATGCCCT
 15 ATCAAAAATAAAATGAGCAGGAACTCCAAATAAACAGTATCTGAGGAAAAAGCTAAACAATACCTAGAAGAATT
 CATCAAACGGCATTAGAGCATCCTGAATTGTCAGAACTTAAACCGTTACTGGGACCAATCCTGTATTGCTGGG
 GCTAACTATGCCGTGGCAGTAAACGTTGCGCAAGTTATCGATAGCGAAACAGCTGATAATTGAAAGACA
 ACTGCTGCTCTTCGATACTCCTGGTATCGTAGCGTAATGGCATTGCAAGCGGCCCTACCCACAATACA
 GAAGAGATAGTGGCACAAATCAATAGCTTATCGTCTTAATGGTGTCAAGCTATTCCATTGGTAGGAGAGCTA
 20 GTTGATATTGGTTCGCTGCATATAATTTGAGAGAGTATTATCAATTTCAGTGTACATATTGCTAT
 AATCGTCCCGGTATTCTCGGGCATAAAACGCAACCATTCTCATGACGGGTATGCTGTCAAGTGGAAACACT
 GTTGAAGATTGATAATCGAACTGGTTCAAGGGAGAGTGGGACGACATAAAATTACTGCTGAAAATACC
 CCGCTTCAATCGGGGTCTACTACCGACTATTCTGGAAAGCTGGACGTTAAAGTCCAAGACTCATATT
 TCCGTAATGGTCGGAAAATAAGGATGCGTTGAGAGCTATAGACGGTATGTAACTTTGTCGCCCTAAATCT
 25 CCTGTTATGTTGGTAATGGTGTGCATGCAATCTCACGTGGATTTCACAGAACGCTCGGAGAAAATTCAT
 TCTAATGAAATTCTCGCGATTCCATAGGCGTTCTGGTACCAAGAAAACAGTAGATCACACCAAGGTTAATTCT
 AAGCTATCGCTATTTTGAATCAAAGCTGA

SEQ ID NO:2

30 DT-GML1
 ATGGGCGCCGACGACGTCGACTCTCTAAATCTTGATGGAAAACCTTCCTCGTACACGGAACTAAA
 CCTGGTTATGTAGATTCCATTCAAAAAGGTATAACAAAGCAAATCTGGTACACAAGGAATTATGACGATGAT
 TGAAAGGGTTTATAGTACCGACAATAAATACGACGCTGCCGACTCTGTAGATAATGAAAACCGCTCTCT
 GGAAAAGCTGGAGGCCTGGTCAAAGTACGTATCCAGGACTGACGAAGGTTCTGCACATAAAAGTGGATAATGCC
 35 GAAACTATTAAGAAAAGAGTTAGGTTAACGTCACTGAACCGTTGATGGAGCAAGTCGGAACGGAAGAGTTATC
 AAAAGGTTGGTGTGGTCTCGCGTGTAGTGCTCAGCCTCCCTCGCTGAGGGAGTTCTAGCGTTGAATAT
 ATTAATAACTGGGAAACAGGCAGGCTAACGCGTAAAGCGTAAAGCCTGAGGTTAAATTTGAAACCCGTGGAAAACGTGGC
 CAAGATGCGATGTATGAGTATATGGCTCAAGCCTGTGCAGGAAATGGACCATTAGGAATGTTGAGTCAAGGTAGC
 TCATTGTCATGCATAAAATCTGATTGGGATGTCATAAGGGATAAAACTAACAGTATCTGAGGAAAAAGCTAAACAATACCTA
 40 CATGGCCCTATCAAAAATGAGCAGGAAAGTCCAAATAAACAGTATCTGAGGAAAAAGCTAAACAATACCTA
 GAAGAATTTCATCAAACGGCATTAGAGCATCCTGAATTGTCAGAACTTAAACCGTTACTGGGACCAATCCTGTA

TTCGCTGGGCTAACTATCGGGCGTGGCAGTAAACGTTGCGCAAGTTATCGATAGCGAACAGCTGATAATTG
 GAAAAGACAACGTGCTGCTTTGATACTTCCTGGTATCGTAGCGTAATGGCATTGCAGACGGTGCCGTTCAC
 CACAATACAGAAGAGATAGTGGCACAATCAATAGCTTATCGTCTTAATGGTTGCTCAAGCTATTCCATTGGTA
 GGAGAGCTAGTTGATATTGGTTGCTGCATATAATTGTAGAGAGTATTATCAATTATTCAAGTAGTTCAT
 5 AATTCTGATAATCGTCCCCTGGCTATTCTCCCGGATAAAACGAGGCCTCATATGGCACCCAGCACGATGCCAAGC
 CCAAGCACGCAGCCCTGGGAGCATGTGAATGCCATCCAGGAGGCCGGTCTCCTGAACCTGAGTAGAGACACT
 GCTGCTGAGATGAATGAAACAGTAGAAAGTCATCTCAGAAATGTTGACCTCCAGGAGGCCGACCTGCCTACAGACC
 CGCCTGGAGCTGTACAAGCAGGGCTGCGGGCAGCCTCACCAAGCTCAAGGGCCCTTGACCATGATGGCTAGC
 CACTACAAGCAGCACTGCCCTCCAACCCCCGAAACTTCCTGTGCGACCCAGACTATCACCTTGAAAGTTCAA
 10 GAGAACCTGAAGGACTTTCTGCTTGTCACTCCCTTGACTGCTGGGAGCCAGTACAGGAAGCTTGA

SEQ ID NO : 3

DT-GML2

ATGGGCGCCGACGACGTCGACTCTTCTAAATCTTGTGATGGAAAACCTTTCTGTACCAACGGACTAAA
 15 CCTGGTTATGTAGATTCATTCAAAAGGTATACAAAAGCCAAATCTGGTACACAAGGAAATTATGACGATGAT
 TGGAAAGGGTTTATAGTACCGACAATAAACGACGCTGCGGGACTCTGTAGATAATGAAAACCCGCTCTCT
 GGAAAAGCTGGAGGCCTGGTCAAAGTGACGTATCCAGGACTGACGAAGGTTCTGCACTAAAGTGGATAATGCC
 GAAACTATTAAGAAAGAGTTAGGTTAAGTCTCACTGAACCGTTGATGGAGCAAGTCGGAACGGAAGAGTTATC
 AAAAGGTTGGTGTAGGGCTCGCTGTAGTGCTCAGCCTCCCTCGCTGAGGGAGTTCTAGCGTTGAATAT
 20 ATTAATAACTGGAACAGGCAGCGTTAACCGTAGAACCTTGAGATTAATTGAAACCCGTGGAAAACGTGGC
 CAAGATGCGATGTATGAGTATGGCTCAAGCCTGTGCAAGGAAATGGACCATAGGATTATGGGCACAAGGTAGC
 TCATTGTCATGCATAAAATCTGATTGGATGTCATAAGGGATAAAACTAACGACAAAGATAGAGTCTTGAAAGAG
 CATGCCCTATCAAAATAAAATGAGCGAAAGTCCAAATAAACAGTATCTGAGGAAAAGCTAAACAATACCTA
 GAAGAATTTCATCAAACGGCATTAGAGCATCCTGAATTGTCAGAACTAAACCGTTACTGGGACCAATCCTGTA
 25 TTGCTGGGCTAACTATCGGGCGTGGCAGTAAACGTTGCGCAAGTTATCGATAGCGAACAGCTGATAATTG
 GAAAAGACAACGTGCTCTTCGATACTTCCTGGTATCGTAGCGTAATGGCATTGCAGACGGTGCCGTTCAC
 CACAATACAGAAGAGATAGTGGCACAATCAATAGCTTATCGTCTTAATGGTTGCTCAAGCTATTCCATTGGTA
 GGAGAGCTAGTTGATATTGGTTGCTGCATATAATTGTAGAGAGTATTATCAATTATTCAAGTAGTTCAT
 AATTCTGATAATCGTCCCCTGGGAGCATGTGAATGCCATCCAGGAGGCCGGTCTCCTGAACCTGAGTAGAGACACT
 30 CCAAGCACGCAGCCCTGGGAGCATGTGAATGCCATCCAGGAGGCCGGTCTCCTGAACCTGAGTAGAGACACT
 GCTGCTGAGATGAATGAAACAGTAGAAAGTCATCTCAGAAATGTTGACCTCCAGGAGGCCGACCTGCCTACAGACC
 CGCCTGGAGCTGTACAAGCAGGGCTGCGGGCAGCCTCACCAAGCTCAAGGGCCCTTGACCATGATGGCTAGC
 CACTACAAGCAGCACTGCCCTCCAACCCCCGAAACTTCCTGTGCGACCCAGACTATCACCTTGAAAGTTCAA
 GAGAACCTGAAGGACTTTCTGCTTGTCACTCCCTTGACTGCTGGGAGCCAGTACAGGAAGCTTGA

35

SEQ ID NO : 4

DT-GMU2

ATGGGCGCCGACGACGTCGACTCTTCTAAATCTTGTGATGGAAAACCTTTCTGTACCAACGGACTAAA
 CCTGGTTATGTAGATTCATTCAAAAGGTATACAAAAGCCAAATCTGGTACACAAGGAAATTATGACGATGAT
 40 TGAAAGGGTTTATAGTACCGACAATAAACGACGCTGCGGGACTCTGTAGATAATGAAAACCCGCTCTCT
 GGAAAAGCTGGAGGCCTGGTCAAAGTGACGTATCCAGGACTGACGAAGGTTCTGCACTAAAGTGGATAATGCC

GAAACTATTAAGAAAGAGTTAGGTTAAGTCTCACTGAACCGTTGATGGAGCAAGTCGGAACGGAAGAGTTATC
AAAAGGTTCGGTGATGGTCTCGCGTGTAGTGCTCAGCCTCCCTCGTGAGGGGAGTTCTAGCGTTGAATAT
ATTAATAACTGGAACAGGCAGCGTTAAGCGTAGAACATTGAGATTAATTTGAAACCCGTGGAAAACGTGGC
CAAGATGCGATGTATGAGTATATGGCTCAAGCCTGTGCAGGAAATGGAAGTGGAAAGATCAGCAGGTAGCTCATTG
5 TCATGCATAAAATCTTGATTGGATGTCATAAGGGATAAAACTAACAGACAAAGATAGAGTCTTGAAAGAGCATGGC
CCTATCAAAAATAAAATGAGCGAAAGTCCCATAAAACAGTATCTGAGGAAAAAGCTAAACAATACCTAGAAGAA
TTTCATCAAACGGCATTAGAGCATTCTGAATTGTCAGAACCTAAACCGTTACTGGGACCAATCCTGATTGCT
GGGGCTAACTATGCCGGTGGCAGTAAACGTTGCGCAAGTTATCGATAGCGAAACAGCTGATAATTGGAAAAG
ACAACGTGCTCTTCGATACTTCCTGGTATCGTAGCGTAATGGCATTGAGACGGTGCCGTTACCCACAAT
10 ACAGAAAGAGATAGTGGCACAACTAACATAGCTTTATCGTCTTAATGGTTGCTCAAGCTATTCCATTGGTAGGAGAG
CTAGTTGATATTGGTTTCGCTGCATATAATTGAGAGTATTATCAATTATTCAAGTAGTTGCTATAATTGCT
TATAATCGTCCCGGTATTCTCCGGGCATAAAACGAGGCCTCATGGCACCCAGCAGATGCCAAGCCCCAAGC
ACGCAGCCCTGGGAGCATGTGAATGCCATCCAGGAGGCCGGCTCTCCTGAACCTGAGTAGAGACACTGCTGCT
GAGATGAATGAAACAGTAGAAGTCATCTCAGAAATGTTGACCTCCAGGAGGCCACCTGCCTACAGACCCGCTG
15 GAGCTGTACAAGCAGGCCCTGCCGGCAGCCTCACCAAGCTCAAGGGCCCTTGACCATGATGGCTAGCCACTAC
AAGCAGCACTGCCCTCCAACCCGGAAACTCCTGTGCGACCCAGACTATCACCTTGAAAGTTCAAAGAGAAC
CTGAAGGACTTTCTGCTTGTATCCCTTTGACTGCTGGAGCCAGTACAGGAAGCTTGA

SEQ ID NO:5

DT-GMU3

ATGGGCGCCGACGACGTGTCGACTCTCTAAATCTTGTGATGGAAAACCTTTCTCGTACCAACGGGACTAAA
 CCTGGTTATGTAGATTCCATTCAAAAAGGTATACAAAAGCCAAATCTGGTACACAAGGAAATTATGACGATGAT
 5 TGGAAAGGGTTTATAGTACCGACAATAAACGACGCTGCGGGATACTCTGTAGATAATGAAAACCCGCTCTCT
 GGAAAAGCTGGAGGCCTGGTCAAAGTGACGTATCCAGGACTGACGAAGGTTCTCGCACTAAAAGTGGATAATGCC
 GAAACTATTAAGAAAGAGTTAGGTTAAGTCTCACTGAACCGTTGATGGAGCAAGTCGAACGGAAAGAGTTATC
 AAAAGGTTGGTGTAGGTGCTTCGCGTGTAGTGCTCAGCCTCCCTCGCTGAGGGAGTTCTAGCGTTGAATAT
 ATTAATAACTGGAACAGGCAGCGTTAAGCGTAGAACTTGAGATTAATTTGAAACCGTGGAAAACGTGGC
 10 CAAGATGCGATGTATGAGTATATGGCTCAAGCCTGTGCAAGGAAATGGAAGTGGAAAATCAGCAGGTAGCTCATTG
 TCATGCATAAAATCTTGATTGGATGTCATAAGGGATAAAACTAAGACAAAGATAGTGCTTGAAGAGCATGGC
 CCTATCAAAAATGGAGCGAAAGTCCCATAAAACAGTATCTGAGGAAAAGCTAAACAATACCTAGAAGAA
 TTTCATCAAACGGCATTAGAGCATCCTGAATTGTCAGAACTTAAACCGTTACTGGGACCAATCCTGTATTGCT
 GGGGCTAACTATGCGGCGTGGCAGTAAACGTTGCGCAAGTTATCGATAGCGAAACAGCTGATAATTGAAAAG
 15 ACAACTGCTGCTCTTCGATACTCCTGGTATCGGTAGCGTAATGGGATTGCAAGACGGTGCCTCACCAAT
 ACAGAAGAGATAGTGGCACAATCAATAGCTTATCGTCTTAATGGTGTCAAGCTATTCCATTGGTAGGAGAG
 CTAGTTGATATTGGTTCGCTGCATATAATTGTAGAGAGTATTATCAATTATTCAAGTAGTTCATATTGCG
 TATAATCGTCCCGGTATTCTCCGGCATAAAACGAGGCCTCATATGGCACCAAGCAGCATGCCAAGCCCAAGC
 ACGCAGCCCTGGGAGCATGTGAATGCCATCCAGGAGGCCGGCTCTGAACCTGAGTAGAGACACTGCTGCT
 20 GAGATGAATGAAACAGTAGAAGTCATCTCAGAAATGTTGACCTCCAGGAGCCGACCTGCCAACAGACCCGCTG
 GAGCTGTACAAGCAGGGCCTGCGGGCAGCCTCACCAAGCTCAAGGGCCCTGACCATGATGGCTAGCCACTAC
 AAGCAGCACTGCCCTCCAACCCCGAAACTCCTGTGCGACCCAGACTATCACCTTGAAAGTTCAAAGAGAAC
 CTGAAGGACTTCTGCTTGTCACTCCCTTGACTGCTGGAGCCAGTACAGGAAGCTTGA

25 SEQ ID NO:6

DT-EGFL1

ATGGGCGCCGACGACGTGTCGACTCTCTAAATCTTGTGATGGAAAACCTTTCTCGTACCAACGGGACTAAA
 CCTGGTTATGTAGATTCCATTCAAAAAGGTATACAAAAGCCAAATCTGGTACACAAGGAAATTATGACGATGAT
 TGGAAAGGGTTTATAGTACCGACAATAAACGACGCTGCGGGATACTCTGTAGATAATGAAAACCCGCTCTCT
 30 GGAAAAGCTGGAGGCCTGGTCAAAGTGACGTATCCAGGACTGACGAAGGTTCTCGCACTAAAAGTGGATAATGCC
 GAAACTATTAAGAAAGAGTTAGGTTAAGTCTCACTGAACCGTTGATGGAGCAAGTCGAACGGAAAGAGTTATC
 AAAAGGTTGGTGTAGGTGCTTCGCGTGTAGTGCTCAGCCTCCCTCGCTGAGGGAGTTCTAGCGTTGAATAT
 ATTAATAACTGGAACAGGCAGCGTTAAGCGTAGAACTTGAGATTAATTTGAAACCGTGGAAAACGTGGC
 CAAGATGCGATGTATGAGTATATGGCTCAAGCCTGTGCAAGGAAATGGACCATTAGGAATGTTGAGTCAGGTAGC
 35 TCATTGTATGCATAAAATCTTGATTGGGATGTCATAAGGGATAAAACTAAGACAAAGATAGTGCTTGAAGAG
 CATGGCCCTATCAAAAATGAGCGAAAGTCCCATAAAACAGTATCTGAGGAAAAGCTAAACAATACCTA
 GAAGAATTTCATCAAACGGCATTAGAGCATCCTGAATTGTCAGAACTTAAACCGTTACTGGGACCAATCCTGTA
 TTGCGCTGGGCTAACTATGCGGCGTGGCAGTAAACGTTGCGCAAGTTATCGATAGCGAAACAGCTGATAATTG
 GAAAAGACAACGTGCTGCTTTGATACTTCCCTGGTATCGGTAGCGTAATGGCATTGCAAGACGGTGCCTCAC
 40 CACAATACAGAAGAGATAGTGGCACAATCAATAGCTTATCGTCTTAATGGTGTCAAGCTATTCCATTGGTA
 GGAGAGCTAGTTGATATTGGTTCGCTGCATATAATTGTAGAGAGTATTATCAATTATTCAAGTAGTTCAT

AATTCGTATAATCGTCCCGCGTATTCTCCGGGCATAAAACGAGGCCTCATATGAATTCCGATAGCGAGTGTCCCT
 CTGAGTCACGATGGTTACTGTCTACATGACGGCGTCTGTATGTATATTGAGGCTCTAGACAAGTACGCGTGTAAAT
 TCGTTGTTGGCTACATCGGTGAGCGCTGTCAGTATCGAGATCTGAAATGGTGGAACTTAGATAA

5 SEQ ID NO:7

DT-EGFL2

ATGGGCGCCGACGACGTGTCGACTCTCTAAATCTTTGTATGGAAAACCTTTCTCGTACCGACGGACTAAA
 CCTGGTTATGTAGATTCCATTCAAAAGGTATACAAAAGCCAAATCTGGTACACAAGGAAATTATGACGATGAT
 TGGAAAGGGTTTATAGTACCGACAATAAACGACGCTGCGGACTCTGTAGATAATGAAAACCGCTCTCT
 10 GGAAAAGCTGGAGGCCTGGTCAAAGTGACGTATCCAGGACTGACGAAGGTTCTCGCCTAAAGTGGATAATGCC
 GAAACTATTAAGAAAAGAGTTAGGTTAAGTCTCACTGAACCGTTGATGGAGCAAGTCGGAACGGAAGAGTTATC
 AAAAGGTTGGTGTAGGTGCTTCGCGTGTAGTGCTCAGCCTCCCTCGCTGAGGGGAGTTCTAGCGTTGAATAT
 ATTAATAACTGGGAACAGGCAGGCTTAAGCGTAGAACCTGAGATAATTTGAAACCGTGGAAAACGTGGC
 CAAGATGCGATGTATGAGTATATGGCTCAAGCCTGTGCAGGAAATGGACCATTAGGATTATGGCACACAAGTAGC
 15 TCATTGTCATGCATAAAATCTGATTGGGATGTCATAAGGGATAAAACTAAGACAAAGATAAGAGTCTTGAAAGAG
 CATGGCCCTATCAAAATAAAATGAGCGAAAGTCCAATAAACAGTATCTGAGGAAAAGCTAAACAATACCTA
 GAAGAATTTCATCAAACGGCATTAGAGCATTCTGAATTGTCAGAACCTAAACCGTTACTGGGACCAATCCTGTA
 TTCGCTGGGCTAACTATGCGCGTGGCAGTAAACGTTGCGCAAGTTATCGATAGCGAAACAGCTGATAATTG
 GAAAAGACAACGTGCTGCTCTTCGATACTTCCTGGTATCGTAGCGTAATGGCATTGCAAGACGGTGCCTCAC
 20 CACAATACAGAAGAGATAGTGGCACAAATCAATAGCTTTATGTCCTTAATGGTGTCAAGCTATTCCATTGGTA
 GGAGAGCTAGTTGATATTGGTTTCGCTGCATATAATTTGTAGAGAGTATTATCAATTATTCAAGTAGTTCAT
 AATTTCGTATAATCGTCCCGCGTATTCTCCGGGCATAAAACGAGGCCTCATATGAATTCCGATAGCGAGTGTCCCT
 CTGAGTCACGATGGTTACTGTCTACATGACGGCGTCTGTATGTATATTGAGGCTCTAGACAAGTACGCGTGTAAAT
 TCGTTGTTGGCTACATCGGTGAGCGCTGTCAGTATCGAGATCTGAAATGGTGGAACTTAGATAA

25

SEQ ID NO:8

DT-EGFU2

ATGGGCGCCGACGACGTGTCGACTCTCTAAATCTTTGTATGGAAAACCTTTCTCGTACCGACGGACTAAA
 CCTGGTTATGTAGATTCCATTCAAAAGGTATACAAAAGCCAAATCTGGTACACAAGGAAATTATGACGATGAT
 30 TGAAAAGGGTTTATAGTACCGACAATAAACGACGCTGCGGACTCTGTAGATAATGAAAACCGCTCTCT
 GGAAAAGCTGGAGGCCTGGTCAAAGTGACGTATCCAGGACTGACGAAGGTTCTCGCCTAAAGTGGATAATGCC
 GAAACTATTAAGAAAAGAGTTAGGTTAAGTCTCACTGAACCGTTGATGGAGCAAGTCGGAACGGAAGAGTTATC
 AAAAGGTTGGTGTAGGTGCTTCGCGTGTAGTGCTCAGCCTCCCTCGCTGAGGGGAGTTCTAGCGTTGAATAT
 ATTAATAACTGGGAACAGGCAGGCTTAAGCGTAGAACCTGAGATAATTTGAAACCGTGGAAAACGTGGC
 35 CAAGATGCGATGTATGAGTATATGGCTCAAGCCTGTGCAGGAAATGGAAGATCAGCAGGTAGCTCATTG
 TCATGCATAAAATCTGATTGGGATGTCATAAGGGATAAAACTAAGACAAAGATAAGAGTCTTGAAAGAGCATGGC
 CCTATCAAAATAAAATGAGCGAAAGTCCAATAAACAGTATCTGAGGAAAAGCTAAACAATACCTAGAAGAA
 TTTCATCAAACGGCATTAGAGCATTCTGAATTGTCAGAACCTAAACCGTTACTGGGACCAATCCTGTATTGCT
 GGGGCTAACTATGCGCGTGGCAGTAAACGTTGCGCAAGTTATCGATAGCGAAACAGCTGATAATTGGAAAAG
 40 ACAACTGCTGCTCTTCGATACTTCCTGGTATCGTAGCGTAATGGCATTGCAAGACGGTGCCTCACCAAT
 ACAGAAGAGATAGTGGCACAATCAATAGCTTTATGTCCTTAATGGTGTCAAGCTATTCCATTGGTAGGAGAG

CTAGTTGATATTGGTTCGCTGCATATAATTGTAGAGAGTATTATCAATTATTCAAGTAGTCATAATTG
 TATAATCGTCCCGCGTATTCTCCCGGGCATAAAACGAGGCCCTCATATGAATTCCGATAGCAGTGTCCCTGAGT
 CACGATGGTTACTGTCTACATGACGGCGTCTGTATGTATTGAGGCTCTAGACAAGTACCGTGTATTGCGTT
 GTTGGCTACATCGGTGAGCGCTGTCAGTATCGAGATCTGAAATGGTGGGAACCTAGATAA

5

SEQ ID NO: 9

DT - EGFU3

ATGGGCGCCGACGACGTCGACTCTCTAAATCTTGTATGGAAAACCTTTCTCGTACCAACGGACTAAA
 CCTGGTTATGTAGATTCCATTCAAAAGGTATACAAAAGCCAAATCTGGTACACAAGGAAATTATGACGATGAT
 10 TGAAAAGGGTTTATAGTACCGACAATAAACGACGCTGCGGGATACTCTGTAGATAATGAAAACCCGCTCTCT
 GGAAAAGCTGGAGGCCTGGTCAAAGTGACGTATCCAGGACTGACGAAGGTTCTCGCACTAAAAGTGGATAATGCC
 GAAACTATTAAGAAAAGAGTTAGGTTAAGTCTCACTGAACCGTTGATGGAGCAAGTCGGAACGGAAGAGTTATC
 AAAAGGTTGGTGTATGGTCTCGTGTAGTGTCAAGCCTTCCCTCGCTGAGGGAGTTCTAGCGTTGAATAT
 ATTAATAACTGGGAACAGGCAGCGTTAACGCTAGAACCTGAGATTAATTGAAACCCGTGGAAAACGTGGC
 15 CAAGATGCGATGTATGAGTATATGGCTCAAGCCTGTGCAGGAAATGGAAGTGGAAAATCAGCAGGTAGCTCATTG
 TCATGCATAAAATCTGATTGGATGTCATAAGGGATAAAACTAACAGACAAAGATAGAGTCTTGAAAGAGCATGGC
 CCTATCAAAATAAAATGAGCGAAAGTCCAATAAAACAGTATCTGAGGAAAAGCTAAACAATACCTAGAAGAA
 TTTCATCAAACGGCATTAGAGCATCCTGAATTGTCAGAACCTAACCGTTACTGGACCAATCCTGTATTGCT
 GGGGCTAACTATGCGCGTGGCAGTAAACGTTGCGCAAGTTATCGATAGCGAAACAGCTGATAATTGAAAAG
 20 ACAACTGCTGCTTTGATACTTCTGGTATCGTAGCGTAATGGCATTGCAAGACGGTGCCTCACCAAAAT
 ACAGAAGAGAGATAGTGGCACAATCAATAGCTTATCGTCTTAAATGGTGTCAAGCTATTCCATTGGTAGGAGAG
 CTAGTTGATATTGGTTCGCTGCATATAATTGTAGAGAGTATTATCAATTATTCAAGTAGTCATAATTG
 TATAATCGTCCCGCGTATTCTCCCGGGCATAAAACGAGGCCCTCATATGAATTCCGATAGCAGTGTCCCTGAGT
 CACGATGGTTACTGTCTACATGACGGCGTCTGTATGTATTGAGGCTCTAGACAAGTACCGTGTATTGCGTT
 25 GTTGGCTACATCGGTGAGCGCTGTCAGTATCGAGATCTGAAATGGTGGGAACCTAGATAA

SEQ ID NO: 10

DT - IL2L1

ATGGGCGCCGACGACGTCGACTCTCTAAATCTTGTATGGAAAACCTTTCTCGTACCAACGGACTAAA
 CCTGGTTATGTAGATTCCATTCAAAAGGTATACAAAAGCCAAATCTGGTACACAAGGAAATTATGACGATGAT
 TGAAAAGGGTTTATAGTACCGACAATAAACGACGCTGCGGGATACTCTGTAGATAATGAAAACCCGCTCTCT
 GGAAAAGCTGGAGGCCTGGTCAAAGTGACGTATCCAGGACTGACGAAGGTTCTCGCACTAAAAGTGGATAATGCC
 GAAACTATTAAGAAAAGAGTTAGGTTAAGTCTCACTGAACCGTTGATGGAGCAAGTCGGAACGGAAGAGTTATC
 AAAAGGTTGGTGTATGGTCTCGTGTAGTGTCAAGCCTTCCCTCGCTGAGGGAGTTCTAGCGTTGAATAT
 35 ATTAATAACTGGGAACAGGCAGCGTTAACGCTAGAACCTGAGATTAATTGAAACCCGTGGAAAACGTGGC
 CAAGATGCGATGTATGAGTATATGGCTCAAGCCTGTGCAGGAAATGGACCATTAGGAATGTTGAGTCAGGTAGC
 TCATTGTCATGCATAAAATCTGATTGGATGTCATAAGGGATAAAACTAACAGACAAAGATAGAGTCTTGAAAGAG
 CATGGCCCTATCAAAATAAAATGAGCGAAAGTCCAATAAAACAGTATCTGAGGAAAAGCTAAACAATACCTA
 GAAGAATTTCATCAAACGGCATTAGAGCATCCTGAATTGTCAGAACCTAACCGTTACTGGACCAATCCTGTA
 40 TTCGCTGGGCTAACTATGCGCGTGGCAGTAAACGTTGCGCAAGTTATCGATAGCGAAACAGCTGATAATTG
 GAAAAGACAACGTGCTGCTTTGATACTTCTGGTATGGTAGCGTAATGGCATTGCAAGACGGTGCCTCAC

CACAATACAGAAGAGATAGTGGCACAATCAATAGCTTATCGTCTTAATGGTTGCTCAAGCTATTCCATTGGTA
 GGAGAGCTAGTTGATATTGGTTCGCTGCATATAATTGTAGAGAGTATTATCAATTATTCAAGTAGTCAT
 AATTCTATAATCGTCCCCTGCATTCTCCGGGCATAAAACGAGGCCTCATATGGCACCTACTTCAGTTCTACA
 AAGAAAACACAGCTACAACTGGAGCATTACTGCTGGATTTACAGATGATTGAAATGAAATTAAATTACAAG
 5 AATCCCAAACCTACCAGGATGCTCACATTAAAGTTTACATGCCAAGAAGGCCACAGAACTGAAACATCTCAG
 TGTCTAGAAGAAGAACTCAAACCTCTGGAGGAAGTGCTAAATTAGCTCAAAGCAAAACTTCACTTAAGACCC
 AGGGACTTAATCAGCAATATCAACGTAATAGTTCTGGAACTAAAGGGATCTGAAACAAACATTCATGTGTGAATAT
 GCTGATGAGACAGCAACCATTGTAGAATTCTGAACAGATGGATTACCTTGTCAAAGCATCATCTCAACACTG
 ACTTGAA

10

SEQ ID NO:11

DT-IL2L2

ATGGGCGCCGACGACGTCGACTCTCTAAATCTTGTGATGGAAAACCTTCTCGTACCAACGGGACTAAA
 CCTGGTTATGTAGATTCCATTCAAAAAGGTATACAAAAGCCAAATCTGGTACACAAGGAATTATGACGATGAT
 15 TGGAAAGGGTTTATAGTACCGACAATAAACGACGCTGCCGAACTCTGTAGATAATGAAAACCCGCTCTCT
 GGAAAAGCTGGAGGCCTGGTCAAAGTGACGTATCCAGGACTGACGAAGGTTCTCGCACTAAAGTGGATAATGCC
 GAAACTATTAAAGAAAGAGTTAGGTTAAGTCTCACTGAACCGTTGATGGAGCAAGTCGGAACGGAAGAGTTATC
 AAAAGGTTGGTGTGGCTCGCTGTAGTGCTCAGCCTTCCCTCGCTGAGGGAGTTCTAGCGTTGAATAT
 ATTAATAACTGGGAACAGCGAAAGCGTTAACGCTAGAACATTGAGATTAAATTGAAACCCGTGAAAACGTGGC
 20 CAAGATGCGATGTATGAGTATATGGCTCAAGCCTGTGCAGGAATGGACCATAGGATTATGGGACAAGGTAGC
 TCATTGTCATGCATAAAATCTGATTGGGATGTCATAAGGGATAAAACTAACGACAAAGATAGAGTCTTGAAGAG
 CATGGCCCTATCAAAAATGAGCGAAAGTCCAATAAACAGTATCTGAGGAAAAGCTAAACAATACCTA
 GAAGAATTTCATCAAACGGCATTAGAGCATCCTGAATTGTCAGAACCTTACTGGGACCAATCCTGTA
 TTGCTGGGCTAACTATGCGCGTGGCAGTAAACGTTGCGCAAGTTATCGATAGCGAAACAGCTGATAATTG
 25 GAAAAGACAACGTCTGCTCTTCGATACTTCTGGTATCGGTAGCGTAATGGCATTGCAAGACGGTGCCTCAC
 CACAATACAGAAGAGATAGTGGCACAATCAATAGCTTATCGTCTTAATGGTTGCTCAAGCTATTCCATTGGTA
 GGAGAGCTAGTTGATATTGGTTCGCTGCATATAATTGTAGAGAGTATTATCAATTATTCAAGTAGTCAT
 AATTCTATAATCGTCCCCTGCATTCTCCGGGCATAAAACGAGGCCTCATATGGCACCTACTTCAGTTCTACA
 AAGAAAACACAGCTACAACTGGAGCATTACTGCTGGATTTACAGATGATTGAAATGAAATTAAATTACAAG
 30 AATCCCAAACCTACCAGGATGCTCACATTAAAGTTTACATGCCAAGAAGGCCACAGAACTGAAACATCTCAG
 TGTCTAGAAGAAGAACTCAAACCTCTGGAGGAAGTGCTAAATTAGCTCAAAGCAAAACTTCACTTAAGACCC
 AGGGACTTAATCAGCAATATCAACGTAATAGTTCTGGAACTAAAGGGATCTGAAACAAACATTCATGTGTGAATAT
 GCTGATGAGACAGCAACCATTGTAGAATTCTGAACAGATGGATTACCTTGTCAAAGCATCATCTCAACACTG
 ACTTGAA

35

SEQ ID NO:12

DT-IL2U2

ATGGGCGCCGACGACGTCGACTCTCTAAATCTTGTGATGGAAAACCTTCTCGTACCAACGGGACTAAA
 CCTGGTTATGTAGATTCCATTCAAAAAGGTATACAAAAGCCAAATCTGGTACACAAGGAATTATGACGATGAT
 40 TGGAAAGGGTTTATAGTACCGACAATAAACGACGCTGCCGAACTCTGTAGATAATGAAAACCCGCTCTCT
 GGAAAAGCTGGAGGCCTGGTCAAAGTGACGTATCCAGGACTGACGAAGGTTCTCGCACTAAAGTGGATAATGCC

GAAACTATTAAGAAAGAGTTAGGTTAAGTCTCACTGAACCGTTGATGGAGCAAGTCGGAACGGAAGAGTTATC
 AAAAGGTTCGGTGATGGTCTCGCGTGTAGTGCCTAGCCTCCCTCGCTGAGGGAGTTCTAGCGTTGAATAT
 ATTAATAACTGGAACAGCGAAAGCGTTAAGCGTAGAACATTGAGATTAATTTGAAACCCGTGGAAAACGTGGC
 CAAGATGCGATGTATGAGTATATGGCTCAAGCCTGTGCAGGAAATGGAAGTGGAAAGATCAGCAGGTAGCTCATTG
 5 TCATGCATAAAATCTTGATTGGATGTCATAAGGGATAAAACTAACAGACAAAGATAGAGTCTTGAAAGAGCATGGC
 CCTATCAAAAATAAAATGAGCGAAAGTCCCATAAAACAGTATCTGAGGAAAAGCTAAACAATACCTAGAAGAA
 TTTCATCAAACGGCATTAGAGCATTCTGAATTGTCAGAACCTTAAACCGTTACTGGGACCAATCCTGTATCGCT
 GGGGCTAACTATGCGCGTGGCAGTAAACGTTGCAGTATCGATAGCGAAACAGCTGATAATTGGAAAAG
 ACAACTGCTGCTCTTCGATACTTCCTGGTATCGTAGCGTAATGGCATTGCAGACGGTGCCGTTACCACAAAT
 10 ACAGAAGAGATAGTGGCACAACTAACATAGCTTATCGTCTTAATGGTGTCAAGCTATTCCATTGGTAGGAGAG
 CTAGTTGATATTGGTTCTGCTGCATATAATTGAGAGTATTATCAATTATTCAAGTAGTTCTAGTCATAATTG
 TATAATCGTCCCGGTATTCTCCGGGATAAAACGAGGCCTCATATGCCACCTACTCAAGTTCTACAAAGAAA
 ACACAGCTACAACGGCATTACTGCTGGAGCATTACTGCTGGATTACAGATGATTGAAATGAAATTAAATTACAAGAATCCC
 15 AAAACTCACCAGGATGTCACATTAAAGTTACATGCCAAGAAGGCCACAGAACTGAAACATCTCAGTGTCTA
 GAAGAAGAACTCAAACCTCTGGAGGAAGTGTCAAATTAGCTCAAAGCAAAACTTCACTTAAGACCCAGGGAC
 TTAATCAGCAATATCAACGTAATAGTTCTGAACTAAAGGGATCTGAAACAAACATTGATGTGAATATGCTGAT
 GAGACAGCAACCATTGAGAATTCTGAACAGATGGATTACCTTGTCAAAGCATCATCTAACACTGACTTGA

SEQ ID NO: 13

20 DT - IL2U3
 ATGGGCGCCGACGACGTCGACTCTCTAAATCTTGATGGAAAACCTTCTCGTACCAACGGACTAAA
 CCTGGTTATGTAGATTCCATTCAAAGGTATACAAAGCCAAATCTGGTACACAAGGAAATTATGACGATGAT
 TGGAAAGGGTTTATAGTACCGACAATAATACGACGCTGCGGGATACTCTGTAGATAATGAAAACCCGCTCT
 GGAAAAGCTGGAGGCCTGGTCAAAGTGACGTATCCAGGACTGACGAAGGTTCTGCACTAAAGTGGATAATGCC
 25 GAAACTATTAAGAAAGAGTTAGGTTAAGTCTCACTGAACCGTTGATGGAGCAAGTCGGAACGGAAGAGTTATC
 AAAAGGTTCGGTGATGGTCTCGCGTGTAGTGCCTAGCCTCCCTCGCTGAGGGAGTTCTAGCGTTGAATAT
 ATTAATAACTGGAACAGCGAAAGCGTTAAGCGTAGAACATTGAGATTAATTTGAAACCCGTGGAAAACGTGGC
 CAAGATGCGATGTATGAGTATATGGCTCAAGCCTGTGCAGGAAATGGAAGTGGAAAATCAGCAGGTAGCTCATTG
 TCATGCATAAAATCTGATTGGATGTCATAAGGGATAAAACTAACAGACAAAGATAGAGTCTTGAAAGAGCATGGC
 30 CCTATCAAAAATAAAATGAGCGAAAGTCCAATAAAACAGTATCTGAGGAAAAGCTAAACAATACCTAGAAGAA
 TTTCATCAAACGGCATTAGAGCATTCTGAATTGTCAGAACCTTAAACCGTTACTGGGACCAATCCTGTATCGCT
 GGGGCTAACTATGCGCGTGGCAGTAAACGTTGCAGTATCGATAGCGAAACAGCTGATAATTGGAAAAG
 ACAACTGCTGCTCTTCGATACTTCCTGGTATCGTAGCGTAATGGCATTGCAGACGGTGCCGTTACCACAAAT
 ACAGAAGAGATAGTGGCACAATCAATAGCTTATCGCTTTAATGGTGTCAAGCTATTCCATTGGTAGGAGAG
 35 CTAGTTGATATTGGTTCTGCTGCATATAATTGAGAGTATTATCAATTATTCAAGTAGTTCTAGTCATAATTG
 TATAATCGTCCCGGTATTCTCCGGGATAAAACGAGGCCTCATATGCCACCTACTCAAGTTCTACAAAGAAA
 ACACAGCTACAACGGCATTACTGCTGGGTTACAGATGATTGAAATGAAATTAAATTACAAGAATCCC
 AAAACTCACCAGGATGTCACATTAAAGTTACATGCCAAGAAGGCCACAGAACTGAAACATCTCAGTGTCTA
 GAAGAAGAACTCAAACCTCTGGAGGAAGTGTCAAAGCAAAACTTCACTTAAGACCCAGGGAC
 40 TTAATCAGCAATATCAACGTAATAGTTCTGAACTAAAGGGATCTGAAACAAACATTGATGTGAATATGCTGAT
 GAGACAGCAACCATTGAGAATTCTGAACAGATGGATTACCTTGTCAAAGCATCATCTAACACTGACTTGA

SEQ ID NO:14
T7 promoter primer (5' primer for DT constructs)

5 GTAATACGACTCACTATAGGGC

SEQ ID NO:15
3' mutagenic primer for U2 constructs

10 GATTATGCATGACAATGAGCTACCTGCTGATCTTCCACTTCCATTCCTGCACAGGCTTG

SEQ ID NO:16
3' mutagenic primer for U3 constructs

15 GATTATGCATGACAATGAGCTACCTGCTGATTTCCACTTCCATTCCTGCACAGGCTTG

SEQ ID NO:17
3' mutagenic primer for L1 constructs

20 GATTATGCATGACAATGAGCTACCTTGACTAACATCCTAATGGTCCATTCCTGCACAGGCTTG

SEQ ID NO:18
3' mutagenic primer for L2 constructs

25 GATTATGCATGACAATGAGCTACCTTGCCCATAATCCTAATGGTCCATTCCTGCACAGGCTTG

SEQ ID NO:19
MMP substrate octapeptide for L1 constructs

30 GPLGMLSQ

SEQ ID NO:20
MMP substrate octapeptide for L2 constructs

35 GPLGLWAQ

SEQ ID NO:21
uPA substrate hexapeptide for U2 constructs

40 GSGRSA

SEQ ID NO:22
uPA substrate hexapeptide for U3 constructs

45 GSGKSA